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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/680,349	10/07/2003	David H. Walker	D6152CIP2/D1/D	5963

7590 03/24/2005

David L. Parker
FULBRIGHT & JAWORSKI L.L.P.
600 Congress Avenue
Suite 2400
Austin, TX 78701

EXAMINER

MINNIFIELD, NITA M

ART UNIT PAPER NUMBER

1645

DATE MAILED: 03/24/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/680,349

Applicant(s)

WALKER ET AL.

Examiner

N. M. Minnifield

Art Unit

1645

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 05 January 2005.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1 and 2 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1 and 2 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 07 October 2003 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892) 2 sheets
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 1/5/05 3 sheets

- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: _____

DETAILED ACTION

1. Applicant's election of species of SEQ ID NO: 41 and 42 in the reply filed on January 5, 2005 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).
2. Applicants' amendment filed January 5, 2005 is acknowledged and has been entered. Claims 1 and 2 have been amended.
3. Claims 1 and 2 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claims are vague and indefinite in the recitation of "an amino acid sequence". Does Applicant intend for this phrase to define the entire amino acid sequence of SEQ ID NO: 2 or a fragment of the amino acid sequence of SEQ ID NO: 2?
4. The disclosure is objected to because of the following informalities: the continuity data should be updated on page 1 of the specification. Appropriate correction is required.
5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

6. The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) and the Intellectual Property and High Technology Technical Amendments Act of 2002 do not apply when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. Therefore, the prior art date of the reference is determined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

7. Claims 1 and 2 are rejected under 35 U.S.C. 102(e) as being anticipated by Rikihisa et al (6,544,517).

Please note that the effective filing date for the pending claims is September 12, 2000, which is the date the full amino acid sequence of SEQ ID NO: 2 was first disclosed. SEQ ID NO: 2 was first disclosed in 09/660,587 filed September 12, 2000.

Rikihisa et al discloses the claimed amino acid and nucleic acid sequences as set forth in claimed SEQ ID NO: 42 and 41 respectively. SEQ ID NO: 48 and 47 as the same as Applicants' SEQ ID NO: 42 and 47 respectively (see sequence listing in issued patent).

8. Claim 1 is rejected under 35 U.S.C. 102(b) as being anticipated by Rikihisa et al (WO 99/13720), Ohashi et al Infection and Immunity, 1998 or Reddy et al BBRC, 1998.

Rikihisa et al (WO 98/13720), for example, discloses claimed an amino acid sequence of SEQ ID NO: 42. The prior art discloses a 82% sequence match with the claimed SEQ ID NO: 42 (claim 12 and figure 4B). See sequence search result printouts attached.

9. Claims 1 and 2 are rejected under 35 U.S.C. 102(b) as being anticipated by Ohashi et al J. Clinical Microbiology 1998.

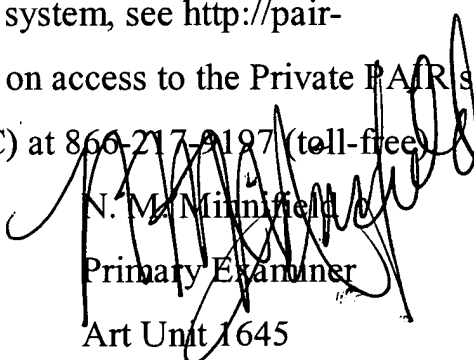
Ohashi et al discloses the claimed amino acid and nucleic acid sequences as set forth in claimed SEQ ID NO: 42 and 41 respectively, please see attached sequence search result printout.

10. Claims 1 and 2 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. Claims 1 and 2, as written, do not sufficiently distinguish over nucleic acids, and proteins as they exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. See *Diamond v. Chakrabarty*, 447 U.S. 303, 206 USPQ 193 (1980). The claims should be amended to indicate the hand of the inventor, e.g., by insertion of "Isolated" or "Purified" as taught and enabled in the specification. See MPEP 2105.

11. No claims are allowed.
12. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.
13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to N. M. Minnifield whose telephone number is 571-272-0860. The examiner can normally be reached on M-F (8:00-5:30) Second Friday Off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette R.F. Smith can be reached on 571-272-0864. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


N. M. Minnifield
Primary Examiner
Art Unit 1645

NMM

March 21, 2005

Please mail w/ Action
3/21/05 MM

Tue Feb 22 10:18:07 2005

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 16:47:35 ; Search time 178 Seconds

(without alignments)
805.518 Million cell updates/sec

Title: US-10-680-349-42

Perfect score: 1662

Sequence: 1 MNVKKILVRSALISLMSILP.....ASVTLVDVGFGEIGMRFTF 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: uniprot_sprot.*
2: uniprot_trembl.*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the change being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1462	100.0	280	2	Q9F476
2	1452	99.3	280	2	Q84HU1
3	1224.5	83.8	283	2	Q8G8D6
4	1217.5	83.3	283	2	Q8G8I2
5	1217.5	83.3	283	2	Q8G8I4
6	1202.5	82.3	283	2	Q8G8I4
7	1124	76.9	282	2	Q9R443
8	1120	76.6	282	2	Q9W441
9	983	67.2	250	2	Q8VTT7
10	665.5	45.5	275	2	Q93DD4
11	655	44.8	276	2	Q8G8I0
12	651	44.3	276	2	Q8G8I7
13	648	44.3	280	2	Q9ZGM9
14	647	44.3	276	2	Q93DD1
15	645.5	44.2	281	2	Q93DD2
16	644.5	44.1	281	2	Q9ACI9
17	644	44.0	280	2	Q8S8I6
18	628	43.0	280	2	Q93DD3
19	621	42.5	288	2	Q9ZGJ2
20	620	42.4	286	2	Q52105
21	605	41.4	280	2	Q52107
22	605	41.4	291	2	Q8G8B3
23	601	41.1	280	2	Q9ADV3
24	600	41.0	280	2	Q9F473
25	599	41.0	291	2	Q8G921
26	598	40.9	291	2	Q8G8G2
27	592	40.5	285	2	Q916Y5
28	589	40.3	287	2	Q8G8G3
29	588	40.2	278	2	Q9R3J3
30	588	40.2	278	2	Q9R8A5
31	588	40.2	278	2	Q9R8A6

ALIGNMENTS

RESULT 1	ID	Q9F476	PRELIMINARY;	PRT;	280 AA.
AC	Q9F476;				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	P28-2 (Major outer membrane protein P30-10).				
GN	Name=p28-2; Synonyms=p30-10;				
OS	Ehrlichia canis.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;				
OC	Anaplasmataceae; Ehrlichia.				
OX	NCBI_TaxID=944;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Jake;				
RX	MEDLINE=9242757; PubMed=10225842;				
RA	McBride J.W., Yu X.J., Walker D.H.;				
RT	"A conserved, transcriptionally active p28 multigene locus of				
RT	Ehrlichia canis."				
RL	Gene 254:245-252(2000).				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Oklaoma;				
RX	MEDLINE=9837112; PubMed=9705412;				
RA	Ohashi N., Unver A., Zhi N., Rikihisa Y.;				
RT	"Cloning and characterization of multigenes encoding the				
RT	immunodominant 30-kilodalton major outer membrane proteins of				
RT	Ehrlichia canis and application of the recombinant protein for				
RT	serodiagnosis."				
RL	J. Clin. Microbiol. 36:2671-2680(1998).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Oklaoma;				
RX	MEDLINE=2153566; PubMed=11254561;				
RA	DOI=10.1128/IAI.69.4.2083-2091.2001;				
RT	Ohashi N., Rikihisa Y., Unver A.;				
RT	"Analysis of transcriptionally active gene clusters of major outer				
RT	membrane protein multigene family in Ehrlichia canis and E.				
RL	infect. Immun. 69:2083-2091(2001).				
RL	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Arizona, California, New Mexico, and Venezuela;				
RX	MEDLINE=22461952; PubMed=12574308;				

RA Felek S., Greene R., Rikhtsa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of E. canis from Diverse Geographic Regions";
RL J. Clin. Microbiol. 41:886-888(2003).
DR EMBL: AF082744; AAC14357.1;
DR EMBL: AF078553; AAC28696.1;
DR EMBL: AF324792; AAC31312.1;
DR EMBL: AF528512; AAC41108.1;
DR EMBL: AF528512; AAC41108.1;
DR EMBL: AF528514; AAC41111.1;
DR EMBL: AF528515; AAC41112.1;
DR InterPro: IPR002566; Surface_Ag_mep4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30962 MW; D1B28B5AF0B6CA3 CRC64;

Query Match 100.0%; Score 1462; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 7, 9e-109;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGYISAKNPSISHRKFSAEET 60
DB 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGYISAKNPSISHRKFSAEET 60
QY 61 PINGTSLTKKVFGLKKDGDITKODFTVAPQIDPQNLLISGSGSIGYMDGPRIELE 120
DB 61 PINGTSLTKKVFGLKKDGDITKODFTVAPQIDPQNLLISGSGSIGYMDGPRIELE 120
QY 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
DB 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
QY 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
DB 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITTFKDLNLFKAYOGKIGISYPIPEVSAPFGYHYHGVINX 240
DB 181 AEGVSFVPYACAGIGADLITTFKDLNLFKAYOGKIGISYPIPEVSAPFGYHYHGVINX 240
QY 241 FEKIPVITPVVLANPAPOTTASVTLVDVYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLANPAPOTTASVTLVDVYFGGEIGMRFTF 280

RESULT 2
Q84HU1 PRELIMINARY; PRT; 280 AA.
AC 084HU1
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Major outer membrane protein.
GN Name: p30-10.
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=944;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Hawaii;
RX MEDLINE=22461952; PubMed=12574308;
RA Felek S., Greene R., Rikhtsa Y.;
RT "Transcriptional Analysis of p30 Major Outer Membrane Protein Genes of
RT Ehrlichia canis in Naturally Infected Ticks and Sequence Analysis of
RT p30-10 of E. canis from Diverse Geographic Regions";
RL J. Clin. Microbiol. 41:886-888(2003).
DR EMBL: AF528513; AAC41110.1;
DR InterPro: IPR002566; Surface_Ag_mep4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 280 AA; 30990 MW; D1B28B14F5BDCA2 CRC64;

Query Match 99.3%; Score 1452; DB 2; Length 280;
Best Local Similarity 99.3%; Pred. No. 5e-108;
Matches 278; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGYISAKNPSISHRKFSAEET 60

DB 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGYISAKNPSISHRKFSAEET 60
QY 61 PINGTSLTKKVFGLKKDGDITKODFTVAPQIDPQNLLISGSGSIGYMDGPRIELE 120
DB 61 PINGTSLTKKVFGLKKDGDITKODFTVAPQIDPQNLLISGSGSIGYMDGPRIELE 120
QY 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
DB 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
QY 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
DB 121 AAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCYDIT 180
QY 181 AEGVSFVPYACAGIGADLITTFKDLNLFKAYOGKIGISYPIPEVSAPFGYHYHGVINX 240
DB 181 AEGVSFVPYACAGIGADLITTFKDLNLFKAYOGKIGISYPIPEVSAPFGYHYHGVINX 240
QY 241 FEKIPVITPVVLANPAPOTTASVTLVDVYFGGEIGMRFTF 280
DB 241 FEKIPVITPVVLANPAPOTTASVTLVDVYFGGEIGMRFTF 280

RESULT 3
Q8GBD6 PRELIMINARY; PRT; 283 AA.
ID 08GBD6
AC 08GBD6
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE 28kDa outer membrane protein gene 14.
OS Ehrlichia chaffeensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=945;
RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;
RA Cheng C., Paddock C.D., Ganta R.R.;
RT "Molecular heterogeneity of Ehrlichia chaffeensis isolates determined
RT by sequence analysis of the 28-kilodalton outer membrane protein genes
RT and other regions of the genome";
RL Infect. Immun. 71:187-195(2003).
DR EMBL: AF479835; AAC12939.1;
DR EMBL: AF479836; AAC12944.1;
DR EMBL: AF479838; AAC12954.1;
DR InterPro: IPR002566; Surface_Ag_mep4.
DR Pfam: PF01617; Surface_Ag_2; 1.
SQ SEQUENCE 283 AA; 31090 MW; D5825DD4DC51C425 CRC64;

Query Match 83.8%; Score 1224.5; DB 2; Length 283;
Best Local Similarity 81.6%; Pred. No. 8e-90;
Matches 231; Conservative 24; Mismatches 25; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGYISAKNPSISHRKFSA 57
DB 1 MNYKKILVRSALISLMSILPYOSFADPVGSRTNDNKEGYISAKNPSISHRKFSA 60
QY 58 EETPINGTSLTKKVFGLKKDGDITKODFTVAPQIDPQNLLISGSGSIGYMDGPRI 117
DB 61 EETPINGTSLTKKVFGLKKDGDITKODFTVAPQIDPQNLLISGSGSIGYMDGPRI 120
QY 118 EIEAAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCY 177
DB 121 EIEAAYQGFNPKNNTNDNDEEYKHPALSRKDMEDQOYVVLKNDGITFMSLWNTCY 180
QY 178 DITAEVSFVPYACAGIGADLITTFKDLNLFKAYOGKIGISYPIPEVSAPFGYHYHGV 237
DB 181 DITAEVSFVPYACAGIGADLITTFKDLNLFKAYOGKIGISYPIPEVSAPFGYHYHGV 240
QY 238 GNKEEKIPVITPVVLANPAPOTTASVTLVDVYFGGEIGMRFTF 280
DB 241 GNKEEKIPVITPVVLANPAPOTTASVTLVDVYFGGEIGMRFTF 283

RESULT 4

us-10-680-349-42.rup

SEQ	SEQUENCE	283 AA;	31042 MW;	A2960DD4DC45942A	CRC64;
Query Match	83.3%;	Score 1217.5;	DB 2;	Length 283;	
Best Local Similarity	81.3%;	Pred. No. 2; 9e-89;			
Matches 230;	Conservative 24;	Mismatches 26;	Indels 3;	Gaps 14;	
QY	1	MNYKKILVRSALISLMSILPQSPFADVGSR--TNDNKEGFYISAKYNPSISHPRKPSA	57		
DB	1	MNYKKILVRSALISLMSILPQSPFADVPTSNDTGINDSKGEFYISVXKNPSISHPRKPSA	60		
QY	58	EEPTINGTNSLITKVFGLKQDGDITTKDDFRRVAPGIDPQNNLISGRSGISGYMDGRI	117		
DB	61	EEPTINGTNTLTKVFGLKQDGDIAQGNDRPTPALPFONNLISGRSGISGYAMDGRRI	120		
QY	118	ELAEAYQOFNDKNTDNDTNGEYXXKPAFALSRKAMEDOOVYVKNQGITFMSLMVNTCY	177		
DB	121	ELAEAYQKFDKAKNDNDTNGSDYTKVYGLSRRLADPKTKVYVKNQGITFMSLMVNTCY	180		
QY	178	DTAEGVSPVPYACAGIGADLITTFKDLNTPAYQKIGISYPTTPEVSAPFGGYHGVY	237		
DB	181	DTAEGVFPFIPYACAGIGADLINFPKDLNTPFYSQKIGISYPTTPEVSAPFGGYHGVY	240		
QY	238	GNKEFKIPVTPPVYVNDAPQTSAYTLVDVYFGSGEIGMRTTF	280		
DB	241	GNFNFKIPVITPVVLEGAPOTTLSALVTITDYGFGSEVGIRPTF	283		
RESULT 6					
ID	085358	PRELIMINARY;	PRT;	283 AA.	
AC	085358	052103;			
DT	01-NOV-1998	(TRENBLrel. 08, Created)			
DT	01-MAR-2003	(TRENBLrel. 23, Last sequence update)			
DT	05-JUL-2004	(TRENBLrel. 27, Last annotation update)			
DE	28kDa outer membrane protein gene 14 (Major outer membrane protein OMP-1B).				
OS	Name=omp-1B;				
ON	Escherichia chaffeensis.				
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;				
OC	Anaplasmataceae; Ehrlichia.				
OX	NCBI_TaxID=945;				
RA	SEQUENCE FROM N.A.				
EX	MEMLINE=96321180; PubMed=9647746; DOI=10.1006/dbrc.1998.8844;				
RA	Reddy G.R., Suleona C.R., Baret A.F., Mahan S.M., Burridge M.U.,				
RA	Alleman A.R.;				
RT	"Molecular characterization of a 28 kDa surface antigen gene family of the tribe Ehrlichiae."				
RL	Biochem. Biophys. Res. Commun. 247:636-643(1998).				
RA	SEQUENCE FROM N.A.				
EX	MEMLINE=22384137; PubMed=12496165; DOI=10.1128/IAI.71.1.187-195.2003;				
RA	Cheng C., Paddock C.D., Ganta R.R.;				
RT	"Molecular heterogeneity of Ehrlichia chaffeensis isolates determined by sequence analysis of the 28-kilodalton outer membrane protein genes and other regions of the genome."				
RL	Infect. Immun. 71:187-195(2003).				
RA	SEQUENCE FROM N.A.				
RA	Cheng C., Paddock C.D., Ganta R.R.;				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
RA	SEQUENCE FROM N.A.				
RC	STRAIN=Arkansas;				
EX	MEMLINE=98084465; PubMed=9423849;				
RA	Ohishi N., Zhi N., Zhang Y., Rikhsia Y.;				
RT	"Immunodominant major outer membrane proteins of Ehrlichia chaffeensis are encoded by a polymorphic multigene family."				
RL	Infect. Immun. 66:132-139(1998).				
RA	SEQUENCE FROM N.A.				
RC	STRAIN=Arkansas;				
EX	MEMLINE=21153566; PubMed=11254561;				

pld. mail w/ action
3/2/05 mm

RX DOI=10.1128/IAI.69.4.2083-2091.2001;
 RA Olash N., Rikhsa Y., Unver A.;
 RT "Analysis of transcriptionally active gene clusters of major outer
 membrane protein multigene family in *Escherichia coli* and *E.*
 RT *chaffeensis*."; 2083-2091 (2001).
 RU Infect. Immun. 69:2083-2091 (2001).
 DR EMBL; AF479833; AAC02929.1; -.
 DR EMBL; U72291; AAC02936.1; -.
 DR EMBL; AF479834; AAC02933.1; -.
 DR InterPro: IPR002566; Surface_Ag_map4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 283 AA; 31017 MW; DCBCE528771C95D CRC64;

Query Match 82.3%; Score 1202.5; DB 2; Length 283;
 Best Local Similarity 79.5%; Pred. No. 4.6e-88;
 Matches 225; Conservative 26; Mismatches 29; Indels 3; Gaps 1;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSR--TNDKGEFYISAKYPSISHPKFS 57
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 DB 61 EEAINGNTSITTKVFGKKGQDIAQSNFRTDPALEFONNLSGFSGISGMDGPR 120
 QY 118 ELBAAYQGFNPKNNDNDNGEYVGFALSRKDMEDQYVVLKNDGTFMSLMVNTCY 177
 DB 121 ELBAAYQGFDAKNPDNDNDNGEYVGFALSRKDMEDQYVVLKNDGTFMSLMVNTCY 180
 QY 178 DITAEVGFVPAACAGIGADLITFKNLKNFAYOGKIGISYPTPEVSATIGYHGV 237
 DB 181 DITAEVGFVPAACAGIGADLITFKNLKNFAYOGKIGISYPTPEVSATIGYHGV 240
 QY 238 GNFKEKIPVITPVVNDAPQTTASVTLVDVGFGEISGRFTF 280
 DB 241 GNFKEKIPVITPVVNDAPQTTASVTLVDVGFGEISGRFTF 283

RESULT 7

Q9R443 PRELIMINARY; PRT; 282 AA.
 AC 09R443;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 05-JUL-2004 (TrEMBLrel. 13, Last sequence update)
 DE Major antigenic protein 1 like protein.
 OS *Cowdria ruminantium*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 NCBI_TaxID=779;

RP SEQUENCE FROM N.A.
 RA MEDLINE=99216274; PubMed=10198207; DOI=10.1006/dbrc.1999.0459;
 RA Salsosa C.R., Mahan S.M., Barber A.F.;
 RT "The map1 gene of *Cowdria ruminantium* is a member of a multigene
 RT family containing both conserved and variable genes."; 2083-2091 (2001).
 RU Biochem. Biophys. Res. Commun. 257:300-305 (1999).
 DR EMBL; AF125274; AAD26343.1; -.
 DR EMBL; AF125277; AAD26349.1; -.
 DR EMBL; AF125278; AAD26351.1; -.
 DR InterPro: IPR002566; Surface_Ag_map4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 282 AA; 31040 MW; 0CB3C65775C8C90 CRC64;

Query Match 76.9%; Score 1124; DB 2; Length 282;
 Best Local Similarity 76.0%; Pred. No. 8.7e-82;
 Matches 215; Conservative 26; Mismatches 38; Indels 4; Gaps 3;

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QY 58 EETPINGNSLTKKVFGLKKDGTITKDDFTFVAAGIDFONNLSGFSGISGMDGPR 117
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 QY 118 ELBAAYQGFNPKNNDNDNGEYVGFALSRKDMEDQYVVLKNDGTFMSLMVNTCY 177
 DB 121 ELBAAYQGFNPKNNDNDNGEYVGFALSRKDMEDQYVVLKNDGTFMSLMVNTCY 179
 QY 178 DITAEVGFVPAACAGIGADLITFKNLKNFAYOGKIGISYPTPEVSATIGYHGV 237
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RESULT 8

Q9MW41 PRELIMINARY; PRT; 282 AA.
 AC 09MW41;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 05-JUL-2004 (TrEMBLrel. 12, Last sequence update)
 DE Major antigenic protein 1 like protein (MAP1-1).
 OS *Cowdria ruminantium*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 NCBI_TaxID=779;

RP SEQUENCE FROM N.A.
 RA MEDLINE=99216274; PubMed=10198207; DOI=10.1006/dbrc.1999.0459;
 RA Salsosa C.R., Mahan S.M., Barber A.F.;
 RT "The map1 gene of *Cowdria ruminantium* is a member of a multigene
 RT family containing both conserved and variable genes."; 2083-2091 (2001).
 RU Biochem. Biophys. Res. Commun. 257:300-305 (1999).
 RP SEQUENCE FROM N.A.
 RA STRAIN=Meigen; von
 RA van Heerden H., Collins N.E., Brayton K.A., Rademeyer C.,
 RA Allsopp B.A.;
 RT "Characterization of a major outer membrane protein multigene family
 RT in *Escherichia coli* and *E. chaffeensis*."; 2083-2091 (2001).
 RU Gene 330:159-168 (2004).
 DR EMBL; AF125276; AAD26347.1; -.
 DR EMBL; AF125275; AAD26345.1; -.
 DR EMBL; AF125277; AAD26349.1; -.
 DR InterPro: IPR002566; Surface_Ag_map4.
 DR Pfam: PF01617; Surface_Ag_2; 1.
 SQ SEQUENCE 282 AA; 31100 MW; 1CB2DA256B2CA990 CRC64;

Query Match 76.6%; Score 1120; DB 2; Length 282;
 Best Local Similarity 75.6%; Pred. No. 1.8e-81;
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 DB 61 EETPINGNSLTKKVFGLKKDGTITKDDFTFVAAGIDFONNLSGFSGISGMDGPR 120
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 DB 121 ELBAAYQGFNPKNNDNDNGEYVGFALSRKDMEDQYVVLKNDGTFMSLMVNTCY 179
 QY 178 DITAEVGFVPAACAGIGADLITFKNLKNFAYOGKIGISYPTPEVSATIGYHGV 237
 DB 180 DITAEVGFVPAACAGIGADLITFKNLKNFAYOGKIGISYPTPEVSATIGYHGV 239
 QY 238 GNFKEKIPVITPVVNDAPQTTASVTLVDVGFGEISGRFTF 280

pls. mail w/ action
3/21/05 MW

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Qy      421 TACTATTAACAATTTTGAATTTCTGTGTAAGATGATGAAAGATGACCAATATGTTGA 480
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Qy      481 CTTAAAAATGACGGATATATCTTTATATGATGATGATTAATCTTGTGATGACATTA 540
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Db      601 ATTTTAAAGACCTCAATCTTAAATTTGCTTACCAAGAAAAATAGGTTATGATACCT 660
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Db      661 ATCAACACAGAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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Db      721 TTGAGAGAGATATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
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RESULT 2
AR303107
LOCUS      AR303107      843 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 47 from patent US 6544517.
ACCESSION AR303107
VERSION    AR303107.1 GI:31691747
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 843)
AUTHORS    Rikihisa, Y. and Ohnishi, N.
TITLE      Outer membrane protein of Ehrlichia canis and Ehrlichia chaffeensis
JOURNAL    Patent: US 6544517-A 47 08-Apr-2003;
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SOURCE     location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e-140;
Matches 840; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      61 TATCAGCTTTTGCAGATCTGTAGGTTCAAGAACTAATGATTAACAAGAGCTTCTAC 120
Db      61 TATCAGCTTTTGCAGATCTGTAGGTTCAAGAACTAATGATTAACAAGAGCTTCTAC 120
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Qy      781 GCTTCAGTACTCTTGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 840
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RESULT 3
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LOCUS      AF528511      906 bp      DNA      linear      BCT 14-FEB-2003
DEFINITION Ehrlichia canis strain Arizona major outer membrane protein
ACCESSION AF528511
VERSION    AF528511.1 GI:28376378
KEYWORDS
SOURCE     Ehrlichia canis
ORGANISM   Ehrlichia canis

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REFERENCE   1 (bases 1 to 906)
AUTHORS    Bacteriophage; Proteobacteria; Alphaproteobacteria; Rickettsiales;
            Anaplasmataceae; Ehrlichia.
TITLE      Felik, S., Greene, R. and Rikihisa, Y.
JOURNAL    Transcriptional Analysis of p30 Major Outer Membrane Protein Genes
            of Ehrlichia canis in Naturally Infected Ticks and Sequence
            Analysis of p30-10 of E. canis from Diverse Geographic Regions
            U. Clin. Microbiol. 41 (2), 886-888 (2003)
MEDLINE    22461952
PUBMED     12574308
REFERENCE   2 (bases 1 to 906)
AUTHORS    Felik, S., Greene, R. and Rikihisa, Y.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUL-2002) Veterinary Biosciences, Ohio State
            University, 1900 Coffey Road, Columbus, OH 43210, USA

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DEFINITION *Escherichia coli* phosphoribosylaminoimidazole carboxylase (*purK*) gene, complete cds; major outer membrane protein gene cluster 2, complete sequence; and u6 gene, partial cds.

ACCESSION AF324792

VERSION AF324792.1 GI:13591681

KEYWORDS

SOURCE *Escherichia coli*

ORGANISM *Bacteria*; *Proteobacteria*; *Alphaproteobacteria*; *Rickettsiales*; *Anaplasmataceae*; *Escherichia*.

REFERENCE 1 (bases 1 to 6913)

AUTHORS Ohashi,N., Unver,A., Zhi,N. and Rikhina,Y.

TITLE Cloning and characterization of multigenes encoding the immunodominant 30-kilodalton major outer membrane proteins of *Escherichia coli* and application of the recombinant protein for serodiagnosis

J Clin Microbiol. 36 (9), 2671-2680 (1998)

MEDLINE 98371112

PUBMED 9705412

REFERENCE 2 (bases 1 to 6913)

AUTHORS	Ohashi, N., Rikihisa, Y. and Unver, A.
TITLE	Analysis of transcriptionally active gene clusters of major outer membrane protein multigene family in <i>Escherichia coli</i> and <i>E. coli</i> .
JOURNAL	Infect. Immun. 69 (4), 2083-2091 (2001)
MEDLINE	21153566
PUBMED	11254561
REFERENCE	3 (bases 1 to 6913)
AUTHORS	Ohashi, N., Rikihisa, Y. and Unver, A.
TITLE	Direct Submission
JOURNAL	Submitted (29-NOV-2000) Veterinary Biosciences, Ohio State University, 1925 Coffey Rd., Columbus, OH 43210, USA
FEATURES	Location/Qualifiers
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ORIGIN

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2/21/05 pm
page 7

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RESULT 8
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LOCUS Ehllichia canis p28 multigene locus, partial sequence.
DEFINITION AP082744 AF168788 AF168789
VERSION AP082744.2 GI:10181081
KEYWORDS
SOURCE Ehllichia canis
ORGANISM Ehllichia canis
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Ehllichia.
REFERENCE 1 (bases 1 to 11329)
McBride,J.W., Yu,X.J. and Walker,D.H.
Molecular cloning of the gene for a conserved major immunoreactive
28-kilodalton protein of Ehllichia canis: a potential
serodiagnostic antigen
Clin. Diagn. Lab. Immunol. 6 (3), 392-399 (1999)
JOURNAL MEDLINE 10225842
PUBMED 99242757
REFERENCE 2 (bases 1 to 11329)
McBride,J.W., Yu,X.J. and Walker,D.H.
A conserved, transcriptionally active p28 multigene locus of
Ehllichia canis
Gene 254 (1-2), 245-252 (2000)
JOURNAL MEDLINE 20432107
PUBMED 10974556
REFERENCE 3 (bases 1 to 11329)
McBride,J.W., Yu,X.J. and Walker,D.H.
Direct Submission
Submitted (07-AUG-1998) Pathology, University of Texas Medical
Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
4 (bases 1 to 11329)
McBride,J.W., Yu,X.J. and Walker,D.H.
Direct Submission
Submitted (04-AUG-2000) Pathology, University of Texas Medical
Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
Sequence update by submitter
On Sep 18, 2000 this sequence version replaced gi:3769522.
REMARK COMMENT
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